
**CERTIFICATE OF MAILING BY "FIRST CLASS MAIL"**


Susan B. Lynch

In the application of:

Serial No.: 10/010,667

Filing Date: 06 December 2001

For: PEPTIDES DERIVED FROM STEAP1
(AS AMENDED)

Examiner: To be assigned

Group Art Unit: To be assigned

REQUEST FOR CORRECTION OF DRAWINGS

Assistant Commissioner for Patents
Washington, D.C. 20231

Dear Sir:

Enclosed are 21 substitute sheets of drawings for Figures 1A, 1B, 1C, 2, 3A, 3B, 4-1, 4-2, 5, 6, 7, 9, 10, 11A, 11B, 14A-B, 15, 16, 17, 19, and 20 in connection with the above-identified application. In addition, please find enclosed a set of drawings showing the proposed changes in red.

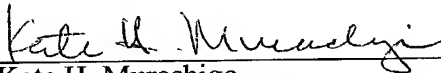
The Figures have been amended to include sequence identification numbers which were inadvertently omitted at the time of filing, and to comply with the appropriate margin requirements as set forth in 37 CFR 1.84(g). Applicants respectfully request the entry of these amendments.

In the unlikely event that the transmittal letter is separated from this request and the U.S. Patent Office determines that an extension and/or other relief is required, applicants petition for any required relief including extensions of time and authorize the Assistant Commissioner to charge the cost of such petitions and/or other fees due in connection with the filing to our **Deposit Account No. 03-1952**. However, the Assistant Commissioner is not authorized to charge the cost of the issue fee to the Deposit Account.

Respectfully submitted,

Dated: March 22, 2002

By:


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FIG. 1A

(SEQ ID NO: 1) 11 20 29 38 47 56
 5' GAG ACT CAC GGT CAA GCT AAG GCG AAG AGT GGG TGG CTG AAG CCA TAC TAT TTT

 65 74 83 92 101 110
 ATA GAA TTA ATG GAA AGC AGA AAA GAC ATC ACA AAC CAA GAA GAA CTT TGG AAA

 (SEQ ID NO: 2) M E S R K D I T N Q E E L W K

 119 128 137 146 155 164
 ATG AAG CCT AGG AGA AAT TTA GAA GAA GAC GAT TAT TTG CAT AAG GAC ACG GGA

 M K P R R N L E E D D Y L H K D T G

 173 182 191 200 209 218
 GAG ACC AGC ATG CTA AAA AGA CCT GTG CTT TTG CAT TTG CAC CAA ACA GCC CAT

 E T S M L K R P V L L H L H Q T A H

 227 236 245 254 263 272
 GCT GAT GAA TTT GAC TGC CCT TCA GAA CTT CAG CAC ACA CAG GAA CTC TTT CCA

 A D E F D C P S E L Q H T Q E L F P

 281 290 299 308 317 326
 CAG TGG CAC TTG CCA ATT AAA ATA GCT GCT ATT ATA GCA TCT CTG ACT TTT CTT

 335 344 353 362 371 380
 TAC ACT CTT CTG AGG GAA GTA ATT CAC CCT TTA GCA ACT TCC CAT CAA CAA TAT

 X T L L R E V I H P L A T S H Q Q Y

 389 398 407 416 425 434
 TTT TAT AAA ATT CCA ATC CTG GTC ATC AAC AAA GTC TTG CCA ATG GTT TCC ATC

 F Y K I P I L V I N K V L P M V S I

 443 452 461 470 479 488
 ACT CTC TTG GCA TTG GTT TAC CTG CCA GGT GTG ATA GCA GCA ATT GTC CAA CTT

 T L L A L V Y L P G V I A A I V Q L

 497 506 515 524 533 542
 CAT AAT GGA ACC AAG TAT AAG AAG TTT CCA CAT TGG TTG GAT AAG TGG ATG TTA

 H N G T K Y K K F P H W L D K W M L

 551 560 569 578 587 596
 ACA AGA AAG CAG TTT GGG CTT CTC AGT TTC TTT TTT GCT GTA CTG CAT GCA ATT

 T R K Q F G L L S F F F A V L H A I

 605 614 623 632 641 650
 TAT AGT CTG TCT TAC CCA ATG AGG CGA TCC TAC AGA TAC AAG TTG CTA AAC TGG

 Y S L S Y P M R R S Y R Y K L L N W

659 668 677 686 695 704 GCA TAT CAA CAG GTC CAA CAA AAT AAA GAA GAT GCC TGG ATT GAG CAT GAT GTT ----- A Y Q Q V Q Q N K E D A W I E H D V																	
713 722 731 740 749 758 TGG AGA ATG GAG ATT TAT GTG TCT CTG GGA ATT GTG GGA TTG GCA ATA CTG GCT ----- W R M E I Y V S L G I V G L A I L A																	
767 776 785 794 803 812 CTG TTG GCT GTG ACA TCT ATT CCA TCT GTG AGT GAC TCT TTG ACA TGG AGA GAA ----- L L A V T S I P S V S D S L T W R E																	
821 830 839 848 857 866 TTT CAC TAT ATT CAG AGC AAG CTA GGA ATT GTT TCC CTT CTA CTG GGC ACA ATA ----- F H Y I O S K L G I V S L L L G T I																	
875 884 893 902 911 920 CAC GCA TTG ATT TTT GCC TGG AAT AAG TGG ATA GAT ATA AAA CAA TTT GTA TGG ----- H A L I F A W N K W I D I K Q F V W																	
929 938 947 956 965 974 TAT ACA CCT CCA ACT TTT ATG ATA GCT GTT TTC CTT CCA ATT GTT GTC CTG ATA ----- Y T P P T F M I A V F L P I V V L I																	
983 992 1001 1010 1019 1028 TTT AAA AGC ATA CTA TTC CTG CCA TGC TTG AGG AAG AAG ATA CTG AAG ATT AGA ----- E K S I L F L P C L R K K I L K I R																	
1037 1046 1055 1064 1073 1082 CAT GGT TGG GAA GAC GTC ACC AAA ATT AAC AAA ACT GAG ATA TGT TCC CAG TTG ----- H G W E D V T K I N K T E I C S Q L																	
1091 1100 1109 1118 1127 1136 TAG AAT TAC TGT TTA CAC ACA TTT TTG TTC AAT ATT GAT ATA TTT TAT CAC CAA ----- * N Y C L H T F L F N I D I F Y H Q																	
1145 1154 1163 1172 1181 1190 CAT TTC AAG TTT GTA TTT GTT AAT AAA ATG ATT ATT CAA GGA AAA AAA AAA AAA ----- H F K F V F V N K M I I Q G K K K K																	

AAA AA 3'

K

FIG. 1B

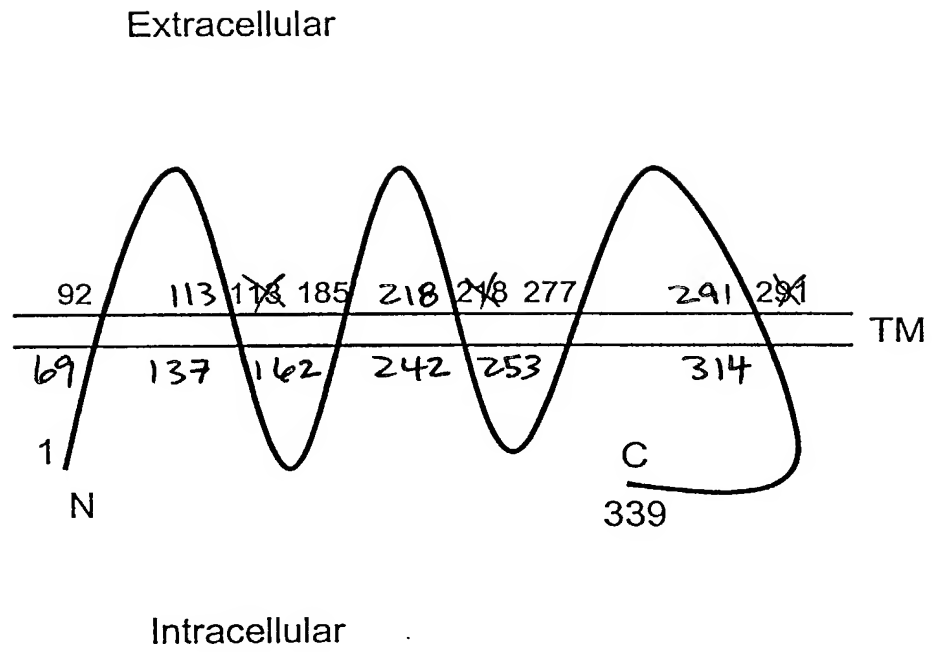


FIG. 1C

5' GGC GGA GGC GGA GGC GGA GGG CGA GGG GCG GGG AGC GCC GCC TGG AGC GCG
GCA GGT CAT ATT GAA CAT TCC AGA TAC CTA TCA TTA CTC GAT GCT GTT GAT
AAC AGC AAG 3' (SEQ ID NO: 3)

FIG. 4-1

GGGGCCCGCACCTCTGGGCAGCAGCGGCAGCCGAGACTCACGGTCAAGCTAAGGCGAAGAGTGGGTGGCTGAAGCC
ATACTATTTTATAGAATTAATGGAAAGCAGAAAAGACATCACAAACCAAGAAGAACTTTGGAAAATGAAGCCTAGG
AGAAATTTAGAAGAAGACGATTATTTGCATAAGGACACGGGAGAGACCAGCATGCTAAAAAGACCTGTGCTTTTGC
ATTTGCACCAAACAGCCCATGCTGATGAATTTGACTGCCCTTCAGAACTTCAGCACACACAGGAACTCTTCCACA
GTGGCACTTGCCAATTAATAATAGCTGCTATTATAGCATCTCTGACTTTTCTTTACACTCTTCTGAGGGAAGTAATT
CACCCCTTAGCAACTTCCCATCAACAATATTTTTATAAAATCCAATCCTGGTCATCAACAAAGTCTTGCCAATGG
TTTCCATCACTCTCTTGGCATTGGTTTACCTGCCAGGTGTGATAGCAGCAATTGTCCAACCTTCATAATGGAACCAA
GTATAAGAAGTTTCCACATTGGTTGGATAAGTGGATGTTAACAAGAAAGCAGTTTGGGCTTCTCAGTTTCTTTTTT
GCTGTACTGCATGCAATTTATAGTCTGTCTTACCCAATGAGGCGATCCTACAGATACAAGTTGCTAAACTGGGCAT
ATCAACAGGTCCAACAAAATAAAGAAGATGCTGGATTGAGCATGATGTTTGGAGAATGGAGATTTATGTGTCTCT
GGGAATTGTGGGATTGGCAATACTGGCTCTGTTGGCTGTGACATCTATTCCATCTGTGAGTGACTCTTTGACATGG
AGAGAAATTTCACTATATTCAGGTAAATAATATATAAAATAACCCTAAGAGGTAAATCTTCTTTTTGTGTTTATGAT
ATAGAATATGTTGACTTTACCCCATAAAAATAACAAATGTTTTTCAACAGCAAAGATCTTATACTTGTTCGAATT
AATAATGTGCTCTCCTGTTGTTTTCCCTATTGCTTCTAATTAGGACAAGTGTTCCTAGACATAAATAAAAGGCAT
TAAATATTTCTTTGTTTTTTTTTTTTGTTTGTGTTGTTTTGTTTGTGTTGTTTTGTTTGTGTTTTTGTGATGAAGTCTCG
CTCTGTTGCCCATGCTGGAGTACAGTGGCAGCATCTCGGCTCACTGCAACCTGCGCCTCCTGGGTTCAGGCGATTCT
TCTTGCCCTCAGCCTCCTGAGTAGCTGGGATTACAGGCACCCATCACCATGTCCAGCTAATTTTTGTATTTTAGTA
GAGACAGGGTTTTCCCATGTTGGCCAGGCTGGTCTCGATCTCCTGACCTCAAATGATCCGCCCACCTCGGCCTCCC
AAAGTGCTGGGATGACAGTTGTGAGCCACCACACTCAGCCTGCTCTTCTAATATTTGAAACTTGTTAGACAATTT
GCTACCCATCTAATGTGATATTTAGGAATCCAATATGCATGGTTTATTATTTCTTAAAAAAATATTCTTTTACC
TGTCACCTGAATTTAGTAATGCCTTTTATGTTACACAACCTTAGCACTTTCAGAAACAAAACTCTCTCCTTGAAA
TAATAGAGTTTTTATCTACCAAAGATATGCTAGTGTCTCATTTCAAAGGCTGCTTTTTCCAGCTTACATTTTATAT
ACTTACTCACTTGAAGTTTCTAAATATTCTTGTAATTTTAAACTATCTCAGATTTACTGAGGTTTATCTTCTGGT
GGTAGATTATCCATAAGAAGAGTGATGTGCCAGAATCACTCTGGGATCCTTGCTGTGACAAGATTCAAAGGACTAAA
TTTAATTCAGTCATGAACACTGCCAATTACCGTTTATGGGTAGACATCTTTGGAAATTTCCACAAGGTCAGACATT
CGCAACTATCCCTTCTACATGTCCACACGTATACTCCAACACTTTATTAGGCATCTGATTAGTTTGAAAGTATGC
CTCCATCTGAATTAGTCCAGTGTGGCTTAGAGTTGGTACAACATTCTCAGAAATTTCTTAATTTTGTAGGTTTCTAG
CCTGATAACCACTGGAGTTCTTTGGTCCTCATTAATAGCTTTCTTCACACATTGCTCTGCCTGTTACACATATGA
TGAACACTGCTTTTTAGACTTCATTAGGAATTTAGGACTGCATCTTGACAACTGAGCCTATTCTACTATATGTAC

FIG. 4-2

1703-011.PC FIG. 4 - SHEET 2 OF 2

ATACCTAGCCCATAAATAGGTATACAATACACATTTGGTAAAATAATTTTCAACCAATGACATGTATTTTCAACT
AGTAACCTAGAAATGTTTCACTTAAATCTGAGAACTGGTTACACTACAAGTTACCTTGGAGATTCATATATGAAA
ACGCAAACCTTAGCTATTTGATTGTATTCCTGAGGACTTAAGAATGCGCCTGAATAATTGTGAGTTCGATTTGTCT
GGCAGGCTAATGACCATTTCCAGTAAAGTGAATAGAGGTCAGAAGTCGTATAAAAGAGGTGTTGTCAGAACACCGT
TGAGATTACATAGGTGAACAACTATTTTAAAGCAACTTTATTTGTGTAGTGACAAAGCATCCCAATGCAGGCTGAA
ATGTTTCATCACATCTCTGGATCTCTCTATTTTGTGCAGACATTGAAAAAATGTTCATATTATTTCCATGTTATC
AGAATATTTGATTTTTTAAAAACATAGGCCAAGTTCATTCCTTCATTATTCATTTATCAAAATCAGAGTGAATCA
CATTAGTCGCCTTCACAACTGATAAAGATCACTGAAGTCAAATTGATTTTTGCTATAATCTTCAATCTACCTATAT
TTAATTGAGAATCTAAATGTACAAATCATTGTGTTGATTCTGCACTGATCCTGCTATAAGTAAGACTCAGTCCCT
GATTTTAGGTATCCTGTGAAAAGCAGAATTAAGACAAATACACAAGAGACAAAGCACAAAAAATAAATATCATAAG
GGGATGAACAAAATGGTGGAGAAAGAGTAGACAAAGTTTTTGATCACCTGCCTTCAAAGAAAGGCTGTGAATTTTG
TTCACCTTAGACAGCTTGGAGACAAGAAATTACCCAAAAGTAAGGTGAGGAGGATAGGCAAAAAGAGCAGAAAGATG
TGAATGGACATTGTTGAGAAATGTGATAGGAAAACAATCATAGATAAAGGATTTCCAAGCAACAGAGCATATCCAG
ATGAGGTAGGATGGGATAAACTCTTATTGAACCAATCTTCACCAATTTTGTGTTTTCTTTTGAGAGCAAGCTAGGA
ATTGTTTCCCTTCTACTGGGCACAATACACGCATTGATTTTTGCCTGGAATAAGTGGATAGATATAAAACAATTTG
TATGGTATACACCTCCAACCTTTTATGATAGCTGTTTTCTTCCAATTGTTGTCTGATATTTAAAGCATACTATT
CCTGCCATGCTTGAGGAAGAAGATACTGAAGATTAGACATGGTTGGGAAGACGTCACCAAAATTAACAAAACCTGAG
ATATGTTCCCAGTTGTAGAACTACTGTTTACACACATTTTGTTCATATTGATATATTTTATCACCAACATTTCA
AGTTTGTATTTGTTAATAAAATGATTATTCAAGGAAAAAAAAAAAAAAAAAAAAA (SEQ ID NO:6)

FIG. 5

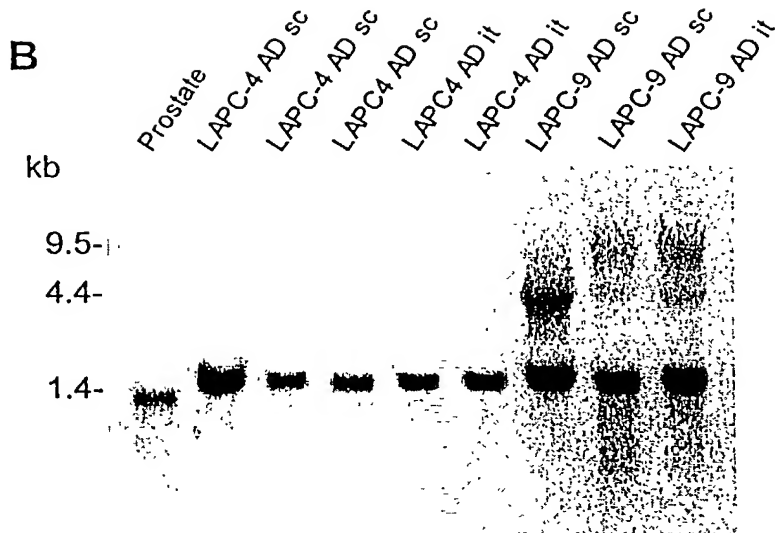
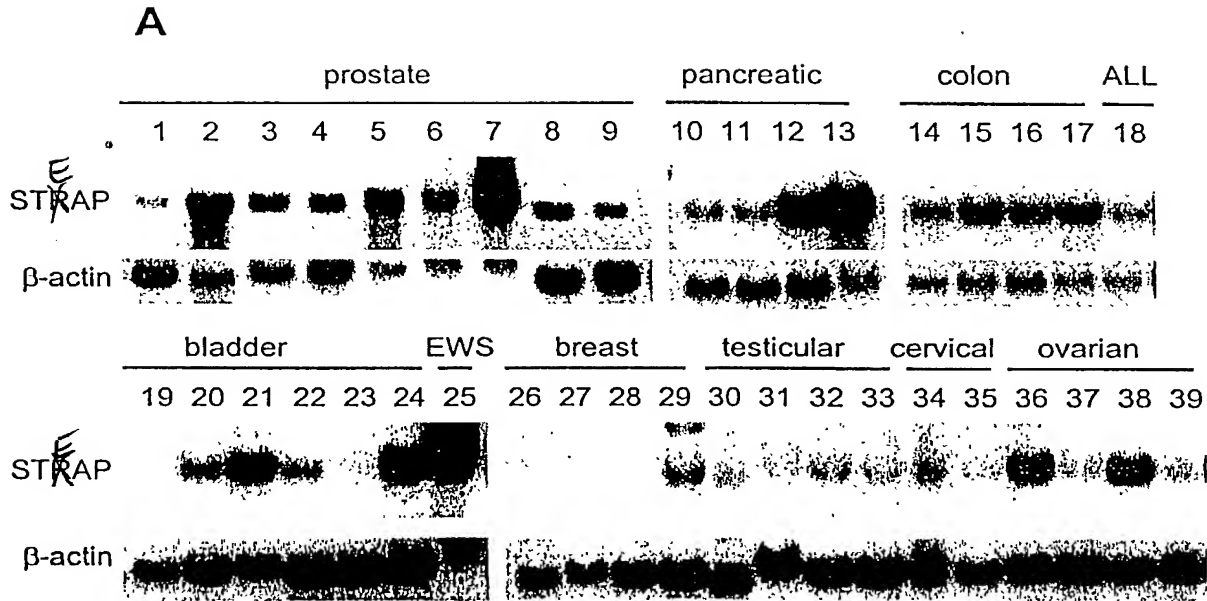


FIG. 6

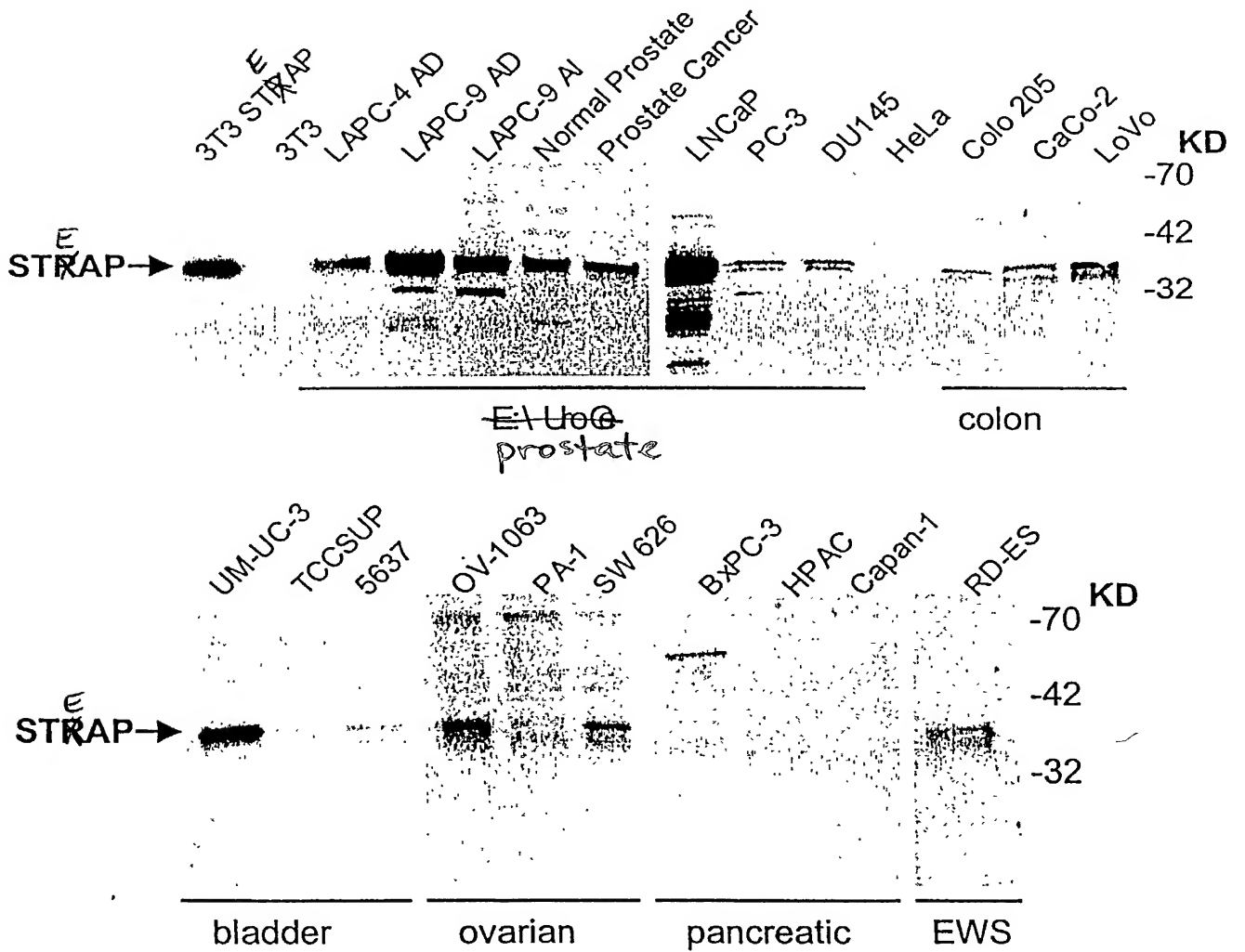


FIG. 7

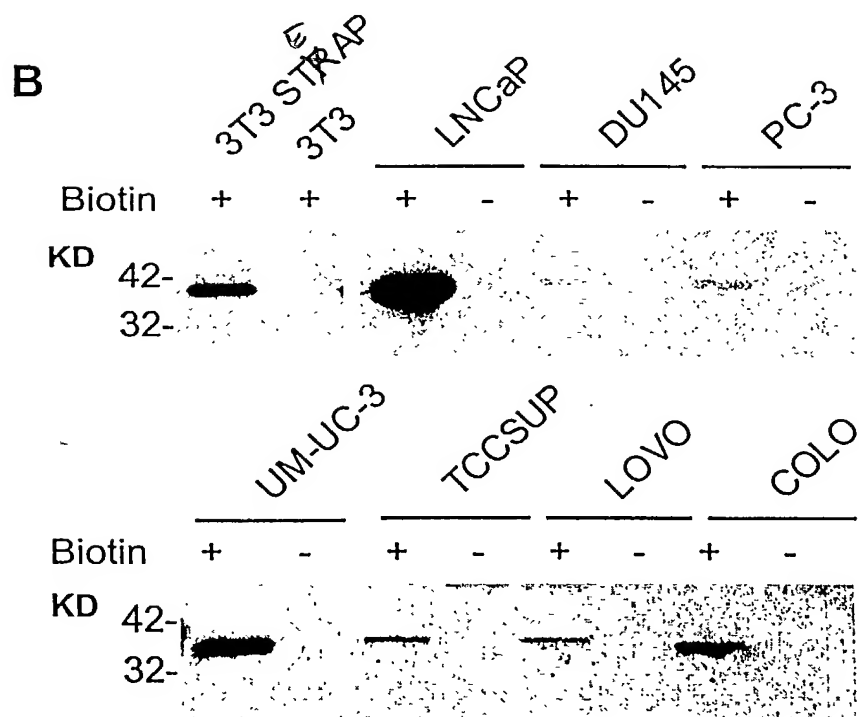
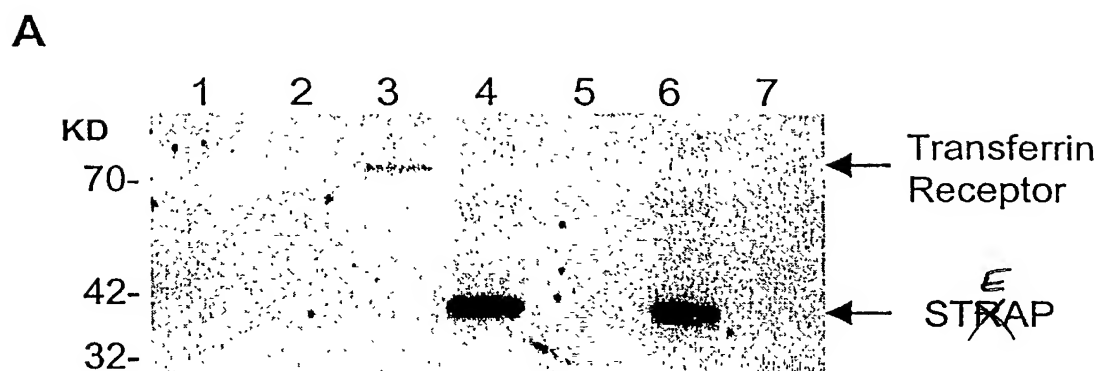


FIG. 9

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5'   10      19      28      37      46      55
    GAC TTT TAC AAA ATT CCT ATA GAG ATT GTG AAT AAA ACC TTA CCT ATA GTT GCC
    --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
    Asp Phe Tyr Lys Ile Pro Ile Glu Ile Val Asn Lys Thr Leu Pro Ile Val Ala

      64      73      82      91      100      109
    ATT ACT TTG CTC TCC CTA GTA TAC CTC GCA GGT CTT CTG GCA GCT GCT TAT CAA
    --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
    Ile Thr Leu Leu Ser Leu Val Tyr Leu Ala Gly Leu Leu Ala Ala Ala Tyr Gln

      118      127      136      145      154      163
    CTT TAT TAC GGC ACC AAG TAT AGG AGA TTT CCA CCT TGG TTG GAA ACC TGG TTA
    --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
    Leu Tyr Tyr Gly Thr Lys Tyr Arg Arg Phe Pro Pro Trp Leu Glu Thr Trp Leu

      172      181      190      199      208      217
    CAG TGT AGA AAA CAG CTT GGA TTA CTA AGT TTT TTC TTC GCT ATG GTC CAT GTT
    --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
    Gln Cys Arg Lys Gln Leu Gly Leu Leu Ser Phe Phe Phe Ala Met Val His Val

      226      235      244      253      262      271
    GCC TAC AGC CTC TGC TTA CCG ATG AGA AGG TCA GAG AGA TAT TTG TTT CTC AAC
    --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
    Ala Tyr Ser Leu Cys Leu Pro Met Arg Arg Ser Glu Arg Tyr Leu Phe Leu Asn

      280      289      298      307      316      325
    ATG GCT TAT CAG CAG GTT CAT GCA AAT ATT GAA AAC TCT TGG AAT GAG GAA GAA
    --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
    Met Ala Tyr Gln Gln Val His Ala Asn Ile Glu Asn Ser Trp Asn Glu Glu Glu

      334      343      352      361      370      379
    GTT TGG AGA ATT GAA ATG TAT ATC TCC TTT GGC ATA ATG AGC CTT GGC TTA CTT
    --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
    Val Trp Arg Ile Glu Met Tyr Ile Ser Phe Gly Ile Met Ser Leu Gly Leu Leu

      388      397      406      415      424      433
    TCC CTC CTG GCA GTC ACT TCT ATC CCT TCA GTG AGC AAT GCT TTA AAC TGG AGA
    --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
    Ser Leu Leu Ala Val Thr Ser Ile Pro Ser Val Ser Asn Ala Leu Asn Trp Arg

      442      451      460      469      478      487
    GAA TTC AGT TTT ATT CAG TCT ACA CTT GGA TAT GTC GCT CTG CTC ATA AGT ACT
    --- --- --- --- --- --- --- --- --- --- --- --- --- --- --- ---
    Glu Phe Ser Phe Ile Gln Ser Thr Leu Gly Tyr Val Ala Leu Leu Ile Ser Thr

      496      505      514
    TTC CAT GTT TTA ATT TAT GGA TGG AAA CGA GCT 3' (SER ID NO: 7)
    --- --- --- --- --- --- --- --- --- --- --- ---
    Phe His Val Leu Ile Tyr Gly Trp Lys Arg Ala (SER ID NO: 8)

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FIG. 10

STAP-2, AA508880 (NCI_CGAP Pr6)
 ggtcgacttttccctttattcctttgtcagagatctgattcatccatatgctagaaaccaacagagtgcacttttaca
 aaattcctatagagattgtgaataaaaaccttacctatagttgccattactttgctctccctagtataccttgcagg
 tcttctggcagctgcttatcaactttattacggcaccaagtataggagatttccaccttgggtggaaacctgggta
 cagtgtagaaaacagcttggattactaagttgtttcttcgctatgggtccatggtgcctacagcctctgcttaccga
 tgagaagggtcagagagat (SEQ ID NO:9)

STAP-2, 98P4B6 SSH fragment
 TTTGCAGCTTTGCAGATACCCAGACTGAGCTGGAAGTGAATTTGTCTTCTATTGACTCTACTTCTTTAAAAGCG
 GCTGCCCCATTACATTCCCTCAGCTGTCTTGCAGTTAGGTGTACATGTGACTGAGTGTGGCCAGTGAGATGAAGTC
 TCCTCAAAGGAAGGCAGCATGTGTCCTTTT (SEQ ID NO:10)

AI139607 (testis EST)
 aagaaggagaatccatttagcacctcctcagcctgggtcagtgattcatatgtggctttgggaatacttgggtttt
 ttctgtttgtactcttgggaatcacttctttgccatctgttagcaatgcagtcactggagagagttccgattttgt
 ccagtcctaaactgggttatttgacctgatcttgtgtacagccacacctgggtgtacggtgggaagagattcctc
 agcccttcaaactcagatgggtatcttctgcagcctacgtgttagggcttatcattccttgcactgtgctgggtga
 tcaagtttgtcctaatacatgccatgtgtagacaacaccttacaaggatccgccagggctgggaaaggaactcaaa
 acactagaaaaagcattgaatggaaaatcaatatttaaaacaaagttcaatttagctggaaaaaa (SEQ ID NO:11)

R80991 (placental EST)
 ggccgcgggcanccgctacgacctgggtcaacctggcagtcaggcaggtcttggccanacaagagccacctctgggtg
 aaggaggagggtctggcggtggagatctacctctccctgggagtgctggccctcggcacgttgctccctgctggccg
 tgacctcactgcggtccattgcaaaactcgtcaactggaggagttcagcttcggttcagtcctcactgggtttgt
 ggccntcgtgctgagcacactncacacgctcacctacgggtggacccgcgccttcgaggagagccgctacaagttc
 tacctnccctccaccttcaegntcacgctgctgggtgcctgcttcggttcacctcctgggcaaaagccctgtttntac
 tgcttgcattcagcgnaga (SEQ ID NO:12)

FIG. 11A

STRAP-1	106	FYKIPILVINKVLPVMSITLLALVYLPGVIAAIVQLHNGTKYKKFPHWLDKWMLTRKQFG
STRAP-2	2	FYKIPIEIVNKTLPIVAITLLSLVYLAGLLAAAYQLYYGTYRRFPWLETWLQCRKQLG
		***** *
STRAP-1	166	LLSFFFVAVLHAIYSLSPMRRSYRYKLLNWAYQQVQONKEDAWIEHDVWRMEIYVSLGIV
STRAP-2	62	LLSFFFAMVHVAYSCLPMRRSERYLFNLMAYQQVHANIENSWNEEEVWRIEMYISFGIM
		***** *
STRAP-1	226	GLAILALLAVTSIPSVSDSLTWREFHYIQSKLGIVSLLLGTIHALIFAWN ⁶
STRAP-2	122	SLGLLSLLAVTSIPSVSNALNWREFSFIQSTLGYVALLISTFHVLIYGWKR
		* *

(Portion of SEQ ID: 2)

(Portion of SEQ ID: 8)

FIG. 11B

	15 16	30 31	45 46	60 61	75 76	90
STRAP-1	MESRDIITNOELWK	MKPRRNLEDDYHLK	DTGETSMLKRPVLH	LHQTADADEFDCPSE	LQHTQELFPQWHLPI	KIAAIIASLTFLYTL
STRAP-2	-----	-----	-----	-----	-----	-----
STRAP-3	-----	-----	-----	-----	-----	-----
STRAP-4	-----	-----	-----	-----	-----	-----
	91	105 106	120 121	135 136	150 151	165 166
STRAP-1	LREVIHPLATSHQY	FIKIPILVINKVLP	VSITLLALVILPGVI	AAIVQLHNGTKYKKE	PHWLDKWMLETRKQFG	LLSFFFAVLHAIKYSL
STRAP-2	-----	-----	-----	-----	-----	-----
STRAP-3	-----	-----	-----	-----	-----	-----
STRAP-4	-----	-----	-----	-----	-----	-----
	181	195 196	210 211	225 226	240 241	255 256
STRAP-1	SYPHRSYKYLINM	AYQOVQONKEDAWIE	HDVWRMEIYVSLGIV	GLAILADLAVTSIPS	VSDSLTWREFHYIQS	KLGIVSLDGTIHAL
STRAP-2	CLPHRSERYPLNM	AYQOVHANIENSWNE	BEVWRIEMYLISFGIM	SIGLLSLLAVTSIPS	VSNALNNREFSFQIS	TLGYVALLISTFHVQ
STRAP-3	-----	-----	-----	-----	-----	-----
STRAP-4	-----	-----	-----	-----	-----	-----
	271	285 286	300 301	315 316	330 331	345 346
STRAP-1	IFAWNKWIDIKQFVW	YTPPTFMIAVFLPIV	VLIFPKSILFLFCGRK	KILKIRHGWEDVTKI	NKTEICSQL	339 (SEQ ID NO: 2)
STRAP-2	YVGHKRA	-----	-----	-----	-----	173 (SEQ ID NO: 8)
STRAP-3	VYGGKRFLSPSNLRW	YLPAAVYVGLIIPCT	VLVIKAVLIMPCVDN	TLKIRIQGWERNKSH	-----	128 (Portion of SEQ ID NO: 2)
STRAP-4	TYGHTRAFEESRYKF	YLPPTETXTLLVPCV	RSSNAKALFXLPICQ	P-----	-----	128 (Portion of SEQ ID NO: 8)

11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30 31 32 33 34 35 36 37 38 39 40 41 42 43 44 45 46 47 48 49 50 51 52 53 54 55 56 57 58 59 60 61 62 63 64 65 66 67 68 69 70 71 72 73 74 75 76 77 78 79 80 81 82 83 84 85 86 87 88 89 90 91 92 93 94 95 96 97 98 99 100

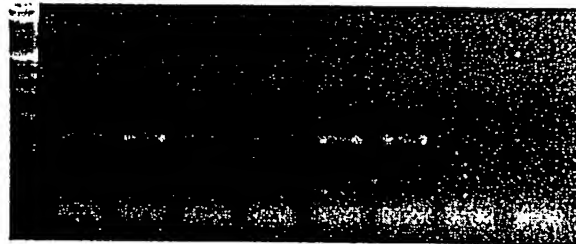
~~FIG. 14~~

FIG. 14A

26x

A

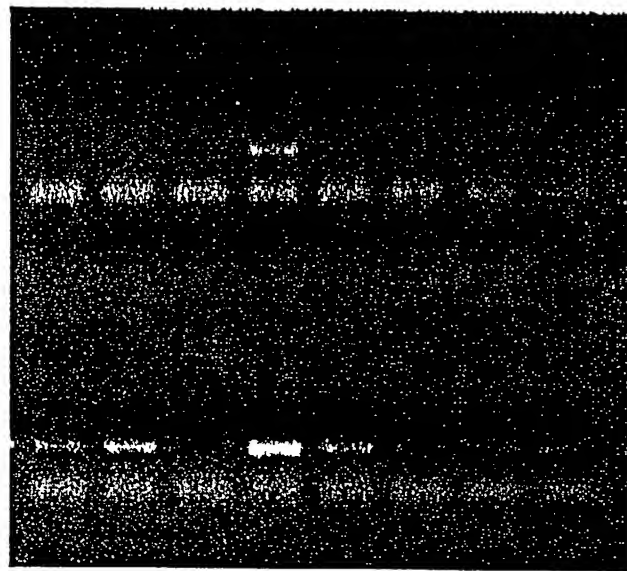
1 2 3 4 5 6 7 8



B

FIG. 14B

1 2 3 4 5 6 7 8



25x

30x

~~A~~

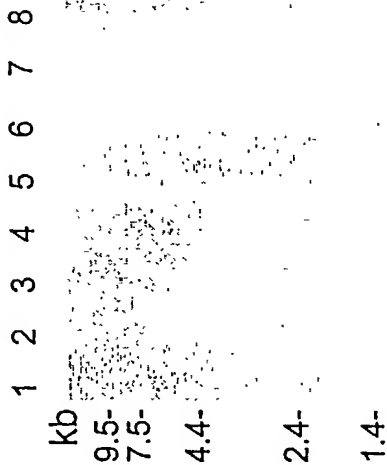
1. Brain
2. Prostate
3. LAPC-4 AD
4. LAPC-4 AI
5. LAPC-9 AD
6. HeLa
7. Murine cDNA
8. Neg. control

~~B~~

1. Colon
2. Ovary
3. Leukocytes
4. Prostate
5. Small Intestine
6. Spleen
7. Testis
8. Thymus

FIG. 15

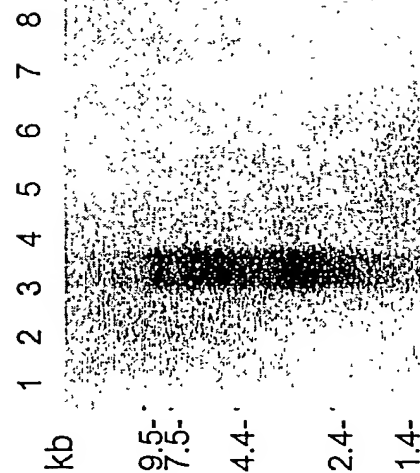
FIG. 15A



A

1. Heart
2. Brain
3. Placenta
4. Lung
5. Liver
6. Skeletal Muscle
7. Kidney
8. Pancreas

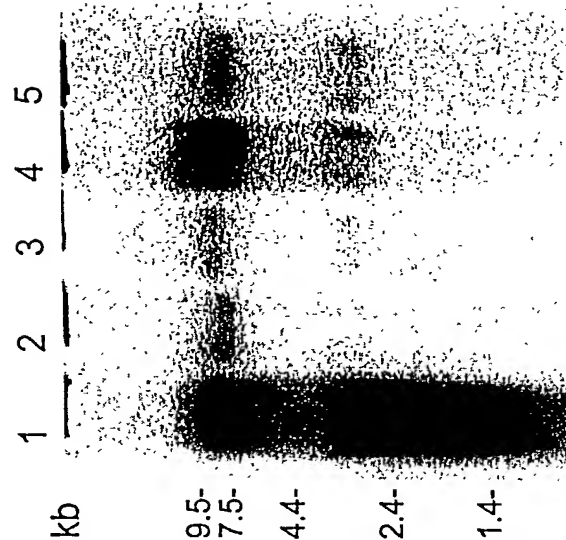
FIG. 15B



B

1. Spleen
2. Thymus
3. Prostate
4. Testis
5. Ovary
6. Small Intestine
7. Colon
8. Leukocytes

FIG. 15C



C

1. Prostate
2. LAPC-4 AD
3. LAPC-4 AI
4. LAPC-9 AD
5. LAPC-9 AI

FIG. 17

GDB Compreher

